

(14)

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,703A

DATE: 11/16/2001
TIME: 15:05:16

Input Set : A:\2001-11-13 3631-0109P CRF.txt
Output Set: N:\CRF3\11162001\I806703A.raw

3 <110> APPLICANT: Steinaa, Lucilla
4 Mouritsen, Soren
5 Gautam, Anand
6 Dalum, Iben
7 Haaning, Jesper
8 Leach, Dana
9 Nielsen, Klaus
10 Karlsson, Gunilla
11 Rasmussen, Peter
13 <120> TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
15 <130> FILE REFERENCE: 3631-0109P
17 <140> CURRENT APPLICATION NUMBER: US 09/806,703A
18 <141> CURRENT FILING DATE: 2001-04-04
20 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00525
21 <151> PRIOR FILING DATE: 1999-10-05
23 <150> PRIOR APPLICATION NUMBER: DK 1998 01261
24 <151> PRIOR FILING DATE: 1998-10-05
26 <150> PRIOR APPLICATION NUMBER: US 60/105,011
27 <151> PRIOR FILING DATE: 1998-10-20
29 <160> NUMBER OF SEQ ID NOS: 41
31 <170> SOFTWARE: PatentIn Ver. 3.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2253
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(2253)
41 <223> OTHER INFORMATION:
43 <220> FEATURE:
W--> 44 <221> NAME/KEY: misc
45 <222> LOCATION: (58)..(2253)
46 <223> OTHER INFORMATION: Human PSM'
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51 1 5 10 15
52 cgc ccg cgc tgg ctg tgc gct ggg gcg ctg gtg ctg gcg ggt ggc ttc 96
53 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
54 20 25 30
55 ttt ctc ctc ggc ttc ctc ggg tgg ttt ata aaa tcc tcc aat gaa 144
56 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
57 35 40 45
58 gct act aac att act cca aag cat aat atg aaa gca ttt ttg gat gaa 192
59 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
60 50 55 60
61 ttg aaa gct gag aac atc aag aag ttc tta tat aat ttt aca cag ata 240

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62	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Phe	Leu	Tyr	Asn	Phe	Thr	Gln	Ile		
63	65					70			75						80		
64	cca	cat	tta	gca	gga	aca	gaa	caa	aac	ttt	cag	ctt	gca	aag	caa	att	288
65	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	Gln	Leu	Ala	Lys	Gln	Ile	
66						85			90					95			
67	caa	tcc	cag	tgg	aaa	gaa	ttt	ggc	ctg	gat	tct	gtt	gag	cta	gca	cat	336
68	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	Asp	Ser	Val	Glu	Leu	Ala	His	
69						100			105				110				
70	tat	gat	gtc	ctg	ttg	tcc	tac	cca	aat	aag	act	cat	ccc	aac	tac	atc	384
71	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	
72						115			120				125				
73	tca	ata	att	aat	gaa	gat	gga	aat	gag	att	ttc	aac	aca	tca	tta	ttt	432
74	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	
75						130			135				140				
76	gaa	cca	cct	cct	cca	gga	tat	gaa	aat	gtt	tcg	gat	att	gta	cca	cct	480
77	Glu	Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	
78						145			150			155		160			
79	ttc	agt	gct	ttc	tct	cct	caa	gga	atg	cca	gag	ggc	gat	cta	gtg	tat	528
80	Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	
81						165			170				175				
82	gtt	aac	tat	gca	cga	act	gaa	gac	ttc	ttt	aaa	ttg	gaa	cgg	gac	atg	576
83	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	
84						180			185			190					
85	aaa	atc	aat	tgc	tct	ggg	aaa	att	gta	att	gcc	aga	tat	ggg	aaa	gtt	624
86	Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	
87						195			200			205					
88	ttc	aga	gga	aat	aag	gtt	aaa	aat	gcc	cag	ctg	gca	ggg	gcc	aaa	gga	672
89	Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Gly	Ala	Lys	Gly		
90						210			215			220					
91	gtc	att	ctc	tac	tcc	gac	cct	gct	gac	tac	ttt	gct	cct	ggg	gtg	aag	720
92	Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
93						225			230			235		240			
94	tcc	tat	cca	gat	ggt	tgg	aat	ctt	cct	gga	ggt	ggt	gtc	cag	cgt	gga	768
95	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly	
96						245			250			255					
97	aat	atc	cta	aat	ctg	aat	ggt	gca	gga	gac	cct	ctc	aca	cca	ggt	tac	816
98	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	
99						260			265			270					
100	cca	gca	aat	gaa	tat	gct	tat	agg	cgt	gga	att	gca	gag	gct	gtt	ggt	864
101	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly	
102						275			280			285					
103	ctt	cca	agt	att	cct	gtt	cat	cca	att	gga	tac	tat	gat	gca	cag	aag	912
104	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys	
105						290			295			300					
106	ctc	cta	gaa	aaa	atg	ggt	ggc	tca	gca	cca	cct	gat	agc	agc	tgg	aga	960
107	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg	
108						305			310			315		320			
109	gga	agt	ctc	aaa	gtt	ccc	tac	aat	gtt	gga	cct	ggc	ttt	act	gga	aac	1008
110	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn	

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111	325	330	335	
112	ttt tct aca caa aaa gtc aag atg cac atc cac tct acc aat gaa gtg			1056
113	Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val			
114	340	345	350	
115	aca aga att tac aat gtg ata ggt act ctc aga gga gca gtg gaa cca			1104
116	Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro			
117	355	360	365	
118	gac aga tat gtc att ctg gga ggt cac cgg gac tca tgg gtg ttt ggt			1152
119	Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly			
120	370	375	380	
121	gtt att gac cct cag agt gga gca gct gtt cat gaa att gtg agg			1200
122	Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg			
123	385	390	395	400
124	agc ttt gga aca ctg aaa aag gaa ggg tgg aga cct aqa aca att			1248
125	Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile			
126	405	410	415	
127	ttg ttt gca agc tgg gat gca gaa gaa ttt ggt ctt ctt ggt tct act			1296
128	Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr			
129	420	425	430	
130	gag tgg gca gag gag aat tca aga ctc ctt caa gag cgt ggc gtg gct			1344
131	Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala			
132	435	440	445	
133	tat att aat gct gac tca tct ata gaa gga aac tac act ctg aga gtt			1392
134	Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val			
135	450	455	460	
136	gat tgt aca ccg ctg atg tac agc ttg gta cac aac cta aca aaa gag			1440
137	Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu			
138	465	470	475	480
139	ctg aaa agc cct gat gaa ggc ttt gaa ggc aaa tct ctt tat gaa agt			1488
140	Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser			
141	485	490	495	
142	tgg act aaa aaa agt cct tcc cca gag ttc agt ggc atg ccc agg ata			1536
143	Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile			
144	500	505	510	
145	agc aaa ttg gga tct gga aat gat ttt gag gtg ttc ttc caa cga ctt			1584
146	Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu			
147	515	520	525	
148	gga att gct tca ggc aga gca cgg tat act aaa aat tgg gaa aca aac			1632
149	Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn			
150	530	535	540	
151	aaa ttc agc ggc tat cca ctg tat cac agt gtc tat gaa aca tat gag			1680
152	Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu			
153	545	550	555	560
154	ttg gtg gaa aag ttt tat gat cca atg ttt aaa tat cac ctc act gtg			1728
155	Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val			
156	565	570	575	
157	gcc cag gtt cga gga ggg atg gtg ttt gag cta gcc aat tcc ata gtg			1776
158	Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val			
159	580	585	590	

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160	ctc	cct	ttt	gat	tgt	cga	gat	tat	gct	gta	gtt	tta	aga	aag	tat	gct	1824
161	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	
162	595							600				605					
163	gac	aaa	atc	tac	agt	att	tct	atg	aaa	cat	cca	cag	gaa	atg	aag	aca	1872
164	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	
165	610							615				620					
166	tac	agt	gta	tca	ttt	gat	tca	ctt	ttt	tct	gca	gta	aag	aat	ttt	aca	1920
167	Tyr	Ser	Val	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	
168	625							630			635		640				
169	gaa	att	gct	tcc	aag	tcc	agt	gag	aga	ctc	cag	gac	ttt	gac	aaa	agc	1958
170	Glu	Ile	Ala	Ser	Lys	Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	
171								645			650		655				
172	aac	cca	ata	gta	tta	aga	atg	atg	aat	gat	caa	ctc	atg	ttt	ctg	gaa	2016
173	Asn	Pro	Ile	Val	Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	
174								660			665		670				
175	aga	gca	ttt	att	gat	cca	tta	ggg	tta	cca	gac	agg	cct	ttt	tat	agg	2064
176	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	
177								675			680		685				
178	cat	gtc	atc	tat	gct	cca	agc	agc	cac	aac	aag	tat	gca	ggg	gag	tca	2112
179	His	Val	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	
180	690							695			700						
181	tcc	cca	gga	att	tat	gat	gct	ctg	ttt	gat	att	gaa	agc	aaa	gtg	gac	2160
182	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	
183	705							710			715		720				
184	cct	tcc	aag	gcc	tgg	gga	gaa	gtg	aag	aga	cag	att	tat	gtt	gca	gcc	2208
185	Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	Ala	
186								725			730		735				
187	tcc	aca	gtg	cag	gca	gct	gca	gag	act	ttg	agt	gaa	gta	gcc	taa	2253	
188	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala			
189								740			745		750				
190	<210>	SEQ	ID	NO:	2												
191	<211>	LENGTH:	750														
192	<212>	TYPE:	PRT														
193	<213>	ORGANISM:	Homo sapiens														
194	<220>	FEATURE:															
195	<221>	NAME/KEY:	misc_feature														
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197	<223> OTHER INFORMATION: The 'Xaa' at location 2 stands for Gly or Trp.																
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201	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly	Gly	Phe	
202					20				25				30				
203	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser	Ser	Asn	Glu	
204																	
205	35				40												
206	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala	Phe	Leu	Asp	Glu	
207																	
208	50				55												
209	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr	Asn	Phe	Thr	Gln	Ile	
210																	
211	65				70												
212																	

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213 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
 214 85 90 95
 215 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
 216 100 105 110
 217 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
 218 115 120 125
 219 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
 220 130 135 140
 221 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
 222 145 150 155 160
 223 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
 224 165 170 175
 225 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
 226 180 185 190
 227 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
 228 195 200 205
 229 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
 230 210 215 220
 231 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
 232 225 230 235 240
 233 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Val Gln Arg Gly
 234 245 250 255
 235 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
 236 260 265 270
 237 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
 238 275 280 285
 239 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
 240 290 295 300
 241 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
 242 305 310 315 320
 243 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
 244 325 330 335
 245 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
 246 340 345 350
 247 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
 248 355 360 365
 249 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
 250 370 375 380
 251 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
 252 385 390 395 400
 253 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
 254 405 410 415
 255 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
 256 420 425 430
 257 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
 258 435 440 445
 259 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
 260 450 455 460
 261 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu

VERIFICATION SUMMARY

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Input Set : A:\2001-11-13 3631-0109P CRF.txt
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L:44 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1

L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2